



10

SEQUENCE LISTING

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<120> NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
USEFUL IN TREATMENT AND DETECTION OF CANCER

<130> 51158-20028.00

<140> 09/942,052
<141> 2001-08-28

<150> 60/228,432
<151> 2000-08-28

<160> 744

<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence: Peptide motif

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<223> Description of Artificial Sequence: Peptide motif

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<223> Description of Artificial Sequence: Peptide motif

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Ala Ala Leu Arg Gly His Phe Cys Leu
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<210> 117

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<223> Description of Artificial Sequence: Peptide motif

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Cys Leu Ser Ser Asp Lys Met Val Cys
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Asp Leu Ser Arg Ser Leu Gly Ala Val
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1 5

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1 5

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1 5

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1 5 10

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1 5 10

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1 5 10

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Ser Leu Met Lys Ile Leu Ser Glu Val Thr
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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

<210> 196
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<400> 196

Ala Asp Ser Val His Leu Ala Trp Asp Leu
1 5 10

<210> 197

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<223> Description of Artificial Sequence: Peptide motif

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Gln Cys His Ala Val Leu Ala Asp Ser Val
1 5 10

<210> 198

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<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 198

Gly Ile Pro Val Gly Phe His Leu Tyr Ser
1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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<223> Description of Artificial Sequence: Peptide motif

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<400> 201
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1 5

<210> 202
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1 5

<210> 203
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<210> 204
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His Leu Tyr Ser Thr His Ala Ala Leu
1 5

<210> 205
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<400> 205
Leu Leu Phe Cys Gly Ser Cys Gly Ile
1 5

<210> 206
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Ser Leu Lys Gly Ser Thr Tyr Asn Leu
1 5

<210> 207
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1 5

<210> 208
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1 5

<210> 209
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1 5

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<400> 210
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1 5

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1 5

<210> 212
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<400> 212
Gly Leu Gly Ala Glu Glu Pro Ala Ala
1 5

<210> 213
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<400> 213
Ala Leu Ala Ala Leu Arg Gly His Phe
1 5

<210> 214

<211> 9
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Val Leu Ala Asp Ser Val His Leu Ala
1 5

<210> 215
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<400> 215
Arg Leu Lys Ser Leu Met Lys Ile Leu
1 5

<210> 216
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Cys Leu Ser Ser Asp Lys Met Val Cys
1 5

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<400> 217
Gly His Phe Cys Leu Ser Ser Asp Lys
1 5

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<223> Description of Artificial Sequence: Peptide motif

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Trp Leu Gln Pro Glu Arg Cys Ala Val
1 5

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<400> 219
Tyr Leu Leu Lys Thr Lys Ala Ile Val
1 5

<210> 220
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1 5

<210> 221
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<400> 221
Ile Val Leu Thr His Asn Arg Leu Lys
1 5

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<400> 222
Lys Ile Val Leu Thr His Asn Arg Leu
1 5

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<400> 223
Lys Ile Ala Glu Leu Lys Glu Lys Ile
1 5

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1 5

<210> 225
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1 5

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<400> 226
Ala Leu Arg Gly His Phe Cys Leu Ser
1 5

<210> 227
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<223> Description of Artificial Sequence: Peptide motif

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<223> Description of Artificial Sequence: Peptide motif

<400> 228
Leu Ser Glu Lys Ile Ala Glu Leu Lys
1 5

<210> 229
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1 5

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<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 345
Leu Thr His Asn Arg Leu Lys Ser Leu
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Glu Lys Ile Ala Glu Leu Lys Glu Lys
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Leu Ala Asp Ser Val His Leu Ala Trp
1 5

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1 5

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1 5 10

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1 5 10

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1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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Ser Asp Lys Met Val Cys Tyr Leu Leu Lys
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<223> Description of Artificial Sequence: Peptide motif

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<223> Description of Artificial Sequence: Peptide motif

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<223> Description of Artificial Sequence: Peptide motif

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Val Val Phe Ser Arg Val Thr Asn Asn Val
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<223> Description of Artificial Sequence: Peptide motif

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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<400> 373
Arg Gly Asp Phe Cys Gly Gly Thr Glu Arg
1 5 10

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<400> 374
Ala Ile Val Asn Ala Ser Glu Met Asp Ile
1 5 10

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1 5 10

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1 5 10

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1 5 10

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Val Leu Ala Asp Ser Val His Leu Ala Trp
1 5 10

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1 5 10

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Leu Tyr Ser Thr His Ala Ala Leu Ala Ala
1 5 10

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Phe Gln Cys Ala Gln Cys His Ala Val Leu
1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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Cys Tyr Leu Leu Lys Thr Lys Ala Ile Val
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Ser Cys Gly Ile Pro Val Gly Phe His Leu
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Tyr Ser Thr His Ala Ala Leu Ala Ala Leu
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1 5 10

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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 574
Ala Val Leu Ala Asp Ser Val His Leu Ala
1 5 10

<210> 575
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<400> 575
Ala Val Phe Gln Cys Ala Gln Cys His Ala
1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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Ser Ser Asp Lys Met Val Cys Tyr Leu Leu
1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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Ala Pro Phe Leu Val Gly Ile Glu Gly Ser
1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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1 5 10

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<223> Description of Artificial Sequence: Peptide motif

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Ala Ile Val Asn Ala Ser Glu Met Asp Ile
1 5 10

<210> 581
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<210> 582
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<220>
<223> Description of Artificial Sequence: Peptide motif

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Leu Thr His Asn Arg Leu Lys Ser Leu Met
1 5 10

<210> 583
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Val Val Phe Ser Arg Val Thr Asn Asn Val
1 5 10

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1 5 10

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Ala Leu Arg Gly His Phe Cys Leu Ser Ser
1 5 10

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1 5 10

<210> 588
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Glu Pro Ala Ala Gly Pro Gln Leu Pro Ser
1 5 10

<210> 589
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1 5 10

<210> 590
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Arg Val Thr Asn Asn Val Val Leu Glu Ala
1 5 10

<210> 591
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<212> PRT
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1 5 10

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1 5 10

<210> 593
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Val Cys Tyr Leu Leu Lys Thr Lys Ala Ile
1 5 10

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1 5 10

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Asn Leu Leu Phe Cys Gly Ser Cys Gly Ile
1 5 10

<210> 596
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1 5 10

<210> 597
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Asn Arg Leu Lys Ser Leu Met Lys Ile Leu
1 5 10

<210> 598
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1 5 10

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Ala Gly Leu Gly Ala Glu Glu Pro Ala Ala
1 5 10

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<400> 600
Ala Leu Ala Ala Leu Arg Gly His Phe Cys
1 5 10

<210> 601
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Leu Ser Ser Asp Lys Met Val Cys Tyr
1 5

<210> 602
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Lys Ala Ile Val Asn Ala Ser Glu Met
1 5

<210> 603
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Arg Leu Lys Ser Leu Met Lys Ile Leu
1 5

<210> 604
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Leu Ala Trp Asp Leu Ser Arg Ser Leu
1 5

<210> 605
<211> 9
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1 5

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Gly Ser Cys Gly Ile Pro Val Gly Phe
1 5

<210> 607
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Ser Ser Pro Leu Gly Pro Ala Gly Leu
1 5

<210> 608
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<220>
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Ser Leu Lys Gly Ser Thr Tyr Asn Leu
1 5

<210> 609
<211> 9
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<223> Description of Artificial Sequence: Peptide motif

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Cys Ala Thr Pro Pro Arg Gly Asp Phe
1 5

<210> 610
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<400> 610
Ala Ala Leu Arg Gly His Phe Cys Leu
1 5

<210> 611
<211> 9
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Phe Ser Arg Val Thr Asn Asn Val Val
1 5

<210> 612
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<400> 612
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1 5

<210> 613

<211> 9
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<400> 613
Ala Ser Phe Thr Thr Ser Met Glu Trp
1 5

<210> 614
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Gly Ile Pro Val Gly Phe His Leu Tyr
1 5

<210> 615
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1 5

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1 5

<210> 617
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<223> Description of Artificial Sequence: Peptide motif

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Thr Ser Met Glu Trp Asp Thr Gln Val
1 5

<210> 618
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<400> 618
Gln Pro Leu Arg His Arg Ser Arg Cys
1 5

<210> 619
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Leu Gln Pro Glu Arg Cys Ala Val Phe
1 5

<210> 620
<211> 9
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<220>
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<400> 620
Lys Ile Val Leu Thr His Asn Arg Leu
1 5

<210> 621
<211> 9
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<220>
<223> Description of Artificial Sequence: Peptide motif

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Asp Gln Ala Ser Phe Thr Thr Ser Met
1 5

<210> 622
<211> 9
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<400> 622
Glu Gly Ser Leu Lys Gly Ser Thr Tyr
1 5

<210> 623
<211> 9
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<220>
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Lys Ile Ala Glu Leu Lys Glu Lys Ile
1 5

<210> 624
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Ser Ser Asp Lys Met Val Cys Tyr Leu
1 5

<210> 625
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<220>
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Ala Val Leu Ala Asp Ser Val His Leu
1 5

<210> 626
<211> 9
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<223> Description of Artificial Sequence: Peptide motif

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Asn Val Val Leu Glu Ala Pro Phe Leu
1 5

<210> 627

<211> 9

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<220>

<223> Description of Artificial Sequence: Peptide motif

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Ala Ala Gly Pro Gln Leu Pro Ser Trp
1 5

<210> 628

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 628

Arg Ala Ile Asp Gln Ala Ser Phe Thr
1 5

<210> 629

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 629

Ala Gly Pro Gln Leu Pro Ser Trp Leu
1 5

<210> 630

<211> 9

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide motif

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Phe Leu Val Gly Ile Glu Gly Ser Leu
1 5

<210> 631
<211> 9
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Cys Gly Ile Pro Val Gly Phe His Leu
1 5

<210> 632
<211> 9
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Ala Leu Ala Ala Leu Arg Gly His Phe
1 5

<210> 633
<211> 9
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Gln Val Val Lys Gly Ser Ser Pro Leu
1 5

<210> 634
<211> 9
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<400> 634
Ser Thr His Ala Ala Leu Ala Ala Leu
1 5

<210> 635
<211> 9
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<220>
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<400> 635
Leu Thr His Asn Arg Leu Lys Ser Leu
1 5

<210> 636
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<400> 636
Arg Ser Leu Gly Ala Val Val Phe Ser
1 5

<210> 637
<211> 9
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<400> 637
Gln Cys Ala Gln Cys His Ala Val Leu
1 5

<210> 638
<211> 9
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His Leu Tyr Ser Thr His Ala Ala Leu
1 5

<210> 639
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Asn Asn Val Val Leu Glu Ala Pro Phe
1 5

<210> 640
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Thr Pro Asp Gln Ser Lys Pro Glu Asn
1 5

<210> 641
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<220>
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Glu Leu Lys Glu Lys Ile Val Leu Thr
1 5

<210> 642
<211> 9
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Asn Ala Ser Glu Met Asp Ile Gln Asn
1 5

<210> 643
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<210> 644
<211> 9
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<220>
<223> Description of Artificial Sequence: Peptide motif

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Gly Ser Leu Lys Gly Ser Thr Tyr Asn
1 5

<210> 645
<211> 9
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<220>
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Gly Ser Thr Tyr Asn Leu Leu Phe Cys
1 5

<210> 646
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Tyr Ser Thr His Ala Ala Leu Ala Ala
1 5

<210> 647
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Ala Ser Glu Met Asp Ile Gln Asn Val
1 5

<210> 648
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<212> PRT
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<223> Description of Artificial Sequence: Peptide motif

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Leu Ala Asp Ser Val His Leu Ala Trp
1 5

<210> 649
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<220>
<223> Description of Artificial Sequence: Peptide motif

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Val Val Leu Glu Ala Pro Phe Leu Val
1 5

<210> 650
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<223> Description of Artificial Sequence: Peptide motif

<400> 650
Phe Cys Gly Gly Thr Glu Arg Ala Ile
1 5

<210> 651
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<220>
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<400> 651
Val Pro Leu Ser Glu Lys Ile Ala Glu Leu
1 5 10

<210> 652
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 652
Phe Ser Arg Val Thr Asn Asn Val Val Leu
1 5 10

<210> 653
<211> 10
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<220>
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<400> 653
Leu Ser Arg Ser Leu Gly Ala Val Val Phe
1 5 10

<210> 654
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 654
Leu Ser Ser Asp Lys Met Val Cys Tyr Leu
1 5 10

<210> 655
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Gly Ser Ser Pro Leu Gly Pro Ala Gly Leu
1 5 10

<210> 656
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<220>
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<400> 656
Tyr Ser Thr His Ala Ala Leu Ala Ala Leu
1 5 10

<210> 657
<211> 10
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<213> Artificial Sequence

<220>
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<400> 657
Gly Ser Leu Lys Gly Ser Thr Tyr Asn Leu
1 5 10

<210> 658
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 658
His Ala Val Leu Ala Asp Ser Val His Leu
1 5 10

<210> 659
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 659
Ala Ala Leu Ala Ala Leu Arg Gly His Phe
1 5 10

<210> 660
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<223> Description of Artificial Sequence: Peptide motif

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Ala Ala Gly Pro Gln Leu Pro Ser Trp Leu
1 5 10

<210> 661
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Thr Ser Met Glu Trp Asp Thr Gln Val Val
1 5 10

<210> 662
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<223> Description of Artificial Sequence: Peptide motif

<400> 662
Leu Ala Ala Leu Arg Gly His Phe Cys Leu
1 5 10

<210> 663
<211> 10
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 663
Ser Leu Lys Gly Ser Thr Tyr Asn Leu Leu
1 5 10

<210> 664
<211> 10
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 664
Ala Pro Phe Leu Val Gly Ile Glu Gly Ser
1 5 10

<210> 665
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<400> 665

Cys Gly Ile Pro Val Gly Phe His Leu Tyr
1 5 10

<210> 666
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 666
Glu Pro Ala Ala Gly Pro Gln Leu Pro Ser
1 5 10

<210> 667
<211> 10
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<400> 667
Leu Thr His Asn Arg Leu Lys Ser Leu Met
1 5 10

<210> 668
<211> 10
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 668
Gln Pro Leu Arg His Arg Ser Arg Cys Ala
1 5 10

<210> 669
<211> 10
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 669
Leu Pro Ser Trp Leu Gln Pro Glu Arg Cys
1 5 10

<210> 670

<211> 10
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 670
Ile Pro Val Gly Phe His Leu Tyr Ser Thr
1 5 10

<210> 671
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 671
Cys Leu Ser Ser Asp Lys Met Val Cys Tyr
1 5 10

<210> 672
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<400> 672
Lys Ser Leu Met Lys Ile Leu Ser Glu Val
1 5 10

<210> 673
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 673
Arg Cys Ala Thr Pro Pro Arg Gly Asp Phe
1 5 10

<210> 674
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<223> Description of Artificial Sequence: Peptide motif

<400> 674

Ser Pro Leu Gly Pro Ala Gly Leu Gly Ala
1 5 10

<210> 675

<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 675

Asn Ala Ser Glu Met Asp Ile Gln Asn Val
1 5 10

<210> 676

<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 676

Gln Ala Ser Phe Thr Thr Ser Met Glu Trp
1 5 10

<210> 677

<211> 10
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<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 677

Ser Ser Asp Lys Met Val Cys Tyr Leu Leu
1 5 10

<210> 678

<211> 10
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<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 678

Asn Asn Val Val Leu Glu Ala Pro Phe Leu
1 5 10

<210> 679
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 679
Ile Ala Glu Leu Lys Glu Lys Ile Val Leu
1 5 10

<210> 680
<211> 10
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 680
Arg Ala Ile Asp Gln Ala Ser Phe Thr Thr
1 5 10

<210> 681
<211> 10
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 681
His Asn Arg Leu Lys Ser Leu Met Lys Ile
1 5 10

<210> 682
<211> 10
<212> PRT
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<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 682
Val Leu Thr His Asn Arg Leu Lys Ser Leu
1 5 10

<210> 683
<211> 10
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<223> Description of Artificial Sequence: Peptide motif

<400> 683

Cys Gly Ser Cys Gly Ile Pro Val Gly Phe
1 5 10

<210> 684

<211> 10

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<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 684

Val Leu Ala Asp Ser Val His Leu Ala Trp
1 5 10

<210> 685

<211> 10

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<223> Description of Artificial Sequence: Peptide motif

<400> 685

Thr Gln Val Val Lys Gly Ser Ser Pro Leu
1 5 10

<210> 686

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 686

Ser Cys Gly Ile Pro Val Gly Phe His Leu
1 5 10

<210> 687

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide motif

<400> 687
His Leu Ala Trp Asp Leu Ser Arg Ser Leu
1 5 10

<210> 688
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 688
Trp Leu Gln Pro Glu Arg Cys Ala Val Phe
1 5 10

<210> 689
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 689
Phe Gln Cys Ala Gln Cys His Ala Val Leu
1 5 10

<210> 690
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 690
Thr Asn Asn Val Val Leu Glu Ala Pro Phe
1 5 10

<210> 691
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 691
Lys Ile Ala Glu Leu Lys Glu Lys Ile Val
1 5 10

<210> 692
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 692
Arg Leu Lys Ser Leu Met Lys Ile Leu Ser
1 5 10

<210> 693
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 693
Pro Pro Arg Gly Asp Phe Cys Gly Gly Thr
1 5 10

<210> 694
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 694
Gln Pro Glu Arg Cys Ala Val Phe Gln Cys
1 5 10

<210> 695
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 695
Asp Ser Val His Leu Ala Trp Asp Leu Ser
1 5 10

<210> 696
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 696
Thr Glu Arg Ala Ile Asp Gln Ala Ser Phe
1 5 10

<210> 697
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 697
Val Cys Tyr Leu Leu Lys Thr Lys Ala Ile
1 5 10

<210> 698
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 698
Ala Ile Val Asn Ala Ser Glu Met Asp Ile
1 5 10

<210> 699
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 699
Asn Leu Leu Phe Cys Gly Ser Cys Gly Ile
1 5 10

<210> 700
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide motif

<400> 700
Ile Gln Asn Val Pro Leu Ser Glu Lys Ile

1

5

10

<210> 701
<211> 496
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Splice variant 1 nucleotide sequence

<400> 701
ttttttttt cctatcttagc tatctcttaa aaacaaaagc catagtaaat gcatcagaga 60
tgatgattca aatgttcct ctatcagaaa agattgcaga ggtaaaattt catgatggtt 120
gtatgctttt ttaaaataca gacaactctt gataacttct accaatgaac ttggggatga 180
tgaatggca tgatgctcaa taatccttt tacttgattt gaccccccatttgaattt 240
taatgaaaaa caaaatacta aaaccacact gtaaggata gttcaggaag aaaggaaaag 300
ctgctcaact gctgcactcc tcattctcc tttgtctgg gaatggatat catcatctt 360
ccatagaggt gtcttcttg caaatacctt gtaattgctc aactgtctca gacataagag 420
tcatgaaaca gttattaaga attcctggcc gggcggtgt gctcacgcct gtaatcccag 480
cactttggcc tcgtgc 496

<210> 702
<211> 83
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 85P1B3 nucleotide sequence

<400> 702
gctatctctt aaaaacaaaaa gccatagtaa atgcatacaga gatggatatt caaaatgttc 60
ctctatcaga aaagattgca gag 83

<210> 703
<211> 83
<212> DNA
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Splice variant 1 nucleotide sequence

<400> 703
gctatctctt aaaaacaaaaa gccatagtaa atgcatacaga gatggatatt caaaatgttc 60
ctctatcaga aaagattgca gag 83

<210> 704
<211> 29
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 85P1B3 peptide
sequence

<400> 704
Tyr Leu Leu Lys Thr Lys Ala Ile Val Asn Ala Ser Glu Met Asp Ile
1 5 10 15

Gln Asn Val Pro Leu Ser Glu Lys Ile Ala Glu Leu Lys
20 25

<210> 705
<211> 165
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Splice variant 1
open reading frame 1 peptide sequence

<220>
<221> MOD_RES
<222> (10)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (15)..(16)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (35)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (56)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (60)..(61)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (74)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (81)..(82)
<223> Unknown amino acid or stop

<220>

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<221> MOD_RES
<222> (87)
<223> Unknown amino acid or stop

<220>
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<222> (122)
<223> Unknown amino acid or stop

<220>
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<222> (139)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (141)..(142)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (146)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (158)
<223> Unknown amino acid or stop

<400> 705
Phe Phe Ser Tyr Leu Ala Ile Ser Xaa Lys Gln Lys Pro Xaa Xaa
      1           5           10           15

Met His Gln Arg Trp Ile Phe Lys Met Phe Leu Tyr Gln Lys Arg Leu
      20          25          30

Gln Arg Xaa Asn Phe Met Met Val Val Cys Phe Phe Lys Ile Gln Thr
      35          40          45

Thr Leu Asp Asn Phe Tyr Gln Xaa Thr Trp Gly Xaa Xaa Asn Gly Met
      50          55          60

Met Leu Asn Asn Pro Phe Tyr Leu Ile Xaa Pro Ser Leu Leu Asn Leu
      65          70          75          80

Xaa Xaa Lys Thr Lys Tyr Xaa Asn His Thr Val Arg Tyr Ser Ser Gly
      85          90          95

Arg Lys Glu Lys Leu Leu Asn Cys Cys Thr Pro Ala Phe Ser Phe Val
      100         105         110

Leu Gly Met Asp Ile Ile Leu Pro Xaa Arg Cys Leu Leu Cys Lys
      115         120         125

Tyr Leu Val Ile Ala Gln Leu Ser Gln Thr Xaa Glu Xaa Xaa Asn Ser
      130         135         140

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Tyr Xaa Glu Phe Leu Ala Gly Arg Gly Gly Ser Arg Leu Xaa Ser Gln
145 150 155 160

His Phe Gly Leu Val
165

<210> 706
<211> 165
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Splice variant 1
open reading frame 2 peptide sequence

<220>
<221> MOD_RES
<222> (6)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (38)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (64)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (72)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (78)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (91)
<223> Unknown amino acid or stop

<220>
<221> MOD_RES
<222> (131)
<223> Unknown amino acid or stop

<400> 706
Phe Phe Phe Pro Ile Xaa Leu Ser Leu Lys Asn Lys Ser His Ser Lys
1 5 10 15

Cys Ile Arg Asp Gly Tyr Ser Lys Cys Ser Ser Ile Arg Lys Asp Cys
20 25 30

Arg Gly Lys Ile Ser Xaa Trp Leu Tyr Ala Phe Leu Lys Tyr Arg Gln
35 40 45

Leu Leu Ile Thr Ser Thr Asn Glu Leu Gly Asp Asp Glu Met Ala Xaa
50 55 60

Cys Ser Ile Ile Leu Phe Thr Xaa Phe Asp Leu Pro Tyr Xaa Ile Cys
65 70 75 80

Asn Glu Lys Gln Asn Thr Lys Thr Thr Leu Xaa Gly Ile Val Gln Glu
85 90 95

Glu Arg Lys Ser Cys Ser Thr Ala Ala Leu Leu His Ser Pro Leu Cys
100 105 110

Trp Glu Trp Ile Ser Ser Ser Cys His Arg Gly Val Phe Phe Ala Asn
115 120 125

Thr Leu Xaa Leu Leu Asn Cys Leu Arg His Lys Ser Asp Glu Thr Val
130 135 140

Ile Lys Asn Ser Trp Pro Gly Val Val Ala His Ala Cys Asn Pro Ser
145 150 155 160

Thr Leu Ala Ser Cys
165

<210> 707

<211> 164

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Splice variant 1
open reading frame 3 peptide sequence

<220>

<221> MOD_RES

<222> (44)

<223> Unknown amino acid or stop

<220>

<221> MOD_RES

<222> (50)..(51)

<223> Unknown amino acid or stop

<220>

<221> MOD_RES

<222> (67)

<223> Unknown amino acid or stop

<220>

<221> MOD_RES

<222> (93)

<223> Unknown amino acid or stop

<400> 707

Phe Phe Phe Leu Ser Ser Tyr Leu Leu Lys Thr Lys Ala Ile Val Asn
1 5 10 15

Ala Ser Glu Met Asp Ile Gln Asn Val Pro Leu Ser Glu Lys Ile Ala
20 25 30

Glu Val Lys Phe His Asp Gly Cys Met Leu Phe Xaa Asn Thr Asp Asn
35 40 45

Ser Xaa Xaa Leu Leu Pro Met Asn Leu Gly Met Met Lys Trp His Asp
50 55 60

Ala Gln Xaa Ser Phe Leu Leu Asp Leu Thr Phe Pro Ile Glu Phe Val
65 70 75 80

Met Lys Asn Lys Ile Leu Lys Pro His Cys Lys Val Xaa Phe Arg Lys
85 90 95

Lys Gly Lys Ala Ala Gln Leu Leu His Ser Cys Ile Leu Leu Cys Ala
100 105 110

Gly Asn Gly Tyr His His Leu Ala Ile Glu Val Ser Ser Leu Gln Ile
115 120 125

Pro Cys Asn Cys Ser Thr Val Ser Asp Ile Arg Val Met Lys Gln Leu
130 135 140

Leu Arg Ile Pro Gly Arg Ala Trp Trp Leu Thr Pro Val Ile Pro Ala
145 150 155 160

Leu Trp Pro Arg

<210> 708

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Illustrative peptide

<400> 708

Lys Asp Glu Leu
1

<210> 709

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6-His tag

<400> 709
His His His His His His
1 5

<210> 710
<211> 14
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Tetanus toxoid peptide

<400> 710
Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1 5 10

<210> 711
<211> 21
<212> PRT
<213> Plasmodium falciparum

<400> 711
Asp Ile Glu Lys Lys Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe
1 5 10 15

Asn Val Val Asn Ser
20

<210> 712
<211> 16
<212> PRT
<213> Streptococcus sp.

<400> 712
Gly Ala Val Asp Ser Ile Leu Gly Gly Val Ala Thr Tyr Gly Ala Ala
1 5 10 15

<210> 713
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Formula peptide

<220>
<221> MOD_RES
<222> (3)
<223> Cyclohexylalanine, Phe or Tyr

<400> 713
Ala Lys Xaa Val Ala Ala Trp Thr Leu Lys Ala Ala Ala
1 5 10

<210> 714
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 714
ttttgatcaa gctttttttt tttttttttt tttttttttt ttt 43

<210> 715
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adaptor

<400> 715
ctaatacga tcactatagg gctcgagcgg ccgccccggc ag 42

<210> 716
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adaptor

<400> 716
gatcctgccc gg 12

<210> 717
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adaptor

<400> 717
gtaatacga tcactatagg gcagcgtggt cgccggccgag 40

<210> 718

<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic adaptor

<400> 718
gatcctcgcc

10

<210> 719
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 719
ctaatacgac tcactatagg gc

22

<210> 720
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 720
tcgagcggcc gccccggcag ga

22

<210> 721
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 721
agcgtggtcg cggccgagga

20

<210> 722
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 722

atatcgccgc gctcgctc gacaa

25

<210> 723
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 723
agccacacgc agtcattgt agaagg

26

<210> 724
<211> 319
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 85P1B3
nucleotide sequence

<400> 724
gatcagagga cacatggac tctgcacatctt aattcctaaa ttacagtca aagacat 60
cagagataag tattatgaat tcaataagaa tctaaagtaa gttcttaagg caaatagcta 120
taaaaagagaa gaatccttag tctctcatct tctaaaaaca gttcacaaa taatttgaa 180
aatcagccta aaggtaata gaaactgcat ttcccctcca ttcttgaagc caatctttt 240
caagaaatga ctaagcagca cctgttgtt aagacagcaa taaagcctga acctgacact 300
caagctttgg tacaggatc 319

<210> 725
<211> 319
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 85P1B3
nucleotide sequence

<400> 725
gatcagagga cacatggac tctgcacatctt aattcctaaa ttacagtca aagacat 60
cagagataag tattatgaat tcaataagaa tctaaagtaa gttcttaagg caaatagcta 120
taaaaagagaa gaatccttag tctctcatct tctaaaaaca gttcacaaa taatttgaa 180
aatcagccta aaggtaata gaaactgcat ttcccctcca ttcttgaagc caatctttt 240
caagaaatga ctaagcagca cctgttgtt aagacagcaa taaagcctga acctgacact 300
caagctttgg tacaggatc 319

<210> 726
<211> 319
<212> DNA
<213> Homo sapiens

<400> 726

gatcagagga cacatggac tctgcattt aattcctaaa tttacagtca aagacatttt 60
 cagagataag tattatgaat tcaataagaa tctaaagtaa gttcttaagg caaatagcta 120
 taaaagagaa gaatccttag tctctcatct tctaaaaaca gcttcacaaa taatttgaa 180
 aatcagccctaa aaggtaaata gaaactgcat ttcccctcca ttcttgaagc caatctttt 240
 caagaaatga ctaagcagca cctgttgg aagacagcaa taaagcctga acctgacact 300
 caagcttgg tacaggatc 319

<210> 727

<211> 1262

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: 85P1B3/OIP5
clone A nucleotide sequence

<220>

<221> CDS

<222> (13)..(699)

<400> 727

ggctgcggga	ag	atg	gcf	gct	cag	ccg	ctg	cgf	cat	cgf	tca	cgt	tgt	gca	51
		Met	Ala	Ala	Gln	Pro	Leu	Arg	His	Arg	Ser	Arg	Cys	Ala	
		1				5					10				

acg	ccg	ccc	cgf	ggf	gac	ttt	tgt	ggf	act	gaf	agg	gcf	att	gac	99
Thr	Pro	Pro	Arg	Gly	Asp	Phe	Cys	Gly	Thr	Glu	Arg	Ala	Ile	Asp	
15						20									
															25

caa	gcf	tct	ttt	acg	acc	tcc	atg	gaf	tgg	gat	acg	cag	gtg	gtg	aag	147
Gln	Ala	Ser	Phe	Thr	Thr	Ser	Met	Glu	Trp	Asp	Thr	Gln	Val	Val	Lys	
30						35					40				45	

ggf	tcc	tcg	ccg	ctc	ggf	ccc	gca	ggf	ctg	ggf	gcf	gat	gag	gaf	cca	gcc	195
Gly	Ser	Ser	Pro	Leu	Gly	Pro	Ala	Gly	Leu	Gly	Ala	Glu	Glu	Pro	Ala		
50						55						60					

gcc	ggf	ccg	cag	ctg	ccg	tct	tgg	ctg	cag	ctg	gaf	agg	tgc	gcf	gtg	243
Ala	Gly	Pro	Gln	Leu	Pro	Ser	Trp	Leu	Gln	Pro	Glu	Arg	Cys	Ala	Val	
65						70					75					

ttc	cag	tgc	gca	cag	tgt	cac	gca	gtg	ctc	gcc	gac	tcg	gtg	cac	ctc	291
Phe	Gln	Cys	Ala	Gln	Cys	His	Ala	Val	Leu	Ala	Asp	Ser	Val	His	Leu	
80							85					90				

gcc	tgg	gaf	ctg	tcg	ccg	tcc	ctc	ggf	gcc	gtg	gtc	ttc	tcc	aga	gtt	339
Ala	Trp	Asp	Leu	Ser	Arg	Ser	Leu	Gly	Ala	Val	Val	Phe	Ser	Arg	Val	
95						100					105					

aca	aat	aac	gtc	gtt	ttg	gaa	gcf	ccc	ttc	cta	gtt	ggf	att	gaa	ggt	387
Thr	Asn	Asn	Val	Val	Leu	Glu	Ala	Pro	Phe	Leu	Val	Gly	Ile	Glu	Gly	
110								115			120			125		

tca	ctc	aaa	ggf	agt	act	tac	aac	ctt	tta	ttc	tgt	ggf	tct	tgt	ggf	435
Ser	Leu	Lys	Gly	Ser	Thr	Tyr	Asn	Leu	Leu	Phe	Cys	Gly	Ser	Cys	Gly	
130								135				140				

att ccc gtt ggt ttc cat ctg tat tct acc cat gct gcc ctg gct gcc		483
Ile Pro Val Gly Phe His Leu Tyr Ser Thr His Ala Ala Leu Ala Ala		
145	150	155
ttg aga ggt cac ttc tgc ctt tcc agt gac aaa atg gtg tgc tat ctc		531
Leu Arg Gly His Phe Cys Leu Ser Ser Asp Lys Met Val Cys Tyr Leu		
160	165	170
tta aaa aca aaa gcc ata gta aat gca tca gag atg gat att caa aat		579
Leu Lys Thr Lys Ala Ile Val Asn Ala Ser Glu Met Asp Ile Gln Asn		
175	180	185
gtt cct cta tca gaa aag att gca gag ctg aaa gag aag ata gtg cta		627
Val Pro Leu Ser Glu Lys Ile Ala Glu Leu Lys Glu Lys Ile Val Leu		
190	195	200
205		
acg cac aat cgc tta aaa tca cta atg aag att ctg agt gaa gtg act		675
Thr His Asn Arg Leu Lys Ser Leu Met Lys Ile Leu Ser Glu Val Thr		
210	215	220
cct gac cag tcc aag cca gaa aac tgatcctgta ccaaagcttg agtgtcaggt		729
Pro Asp Gln Ser Lys Pro Glu Asn		
225		
tcaggcttta ttgctgtctt caacaacagg tgctgcttag tcatttcttg aaaaagattg		789
gcttcaagaa tggagggaa atgcagtttc tatcacctt taggctgatt ttccaaatta		849
tttgtgaagc tgttttaga agatgagaga ctaaggattc ttctctttta tagctattt		909
ccttaagaac ttactttaga ttcttattga attcataata ctatctctg aaaaatgtctt		969
tgactgtaaa tttaggaatt aagatgcaga gtcccatgtg tcctctgatc taaagttgca		1029
tggttggct gaaaatagag ttggcttaa tggtgacttc tattactcct gcatggagca		1089
gttgttatga atactaatac atcactttt aacttctgta aaatacagat cataatattc		1149
tataggtaat gttataaaaa ttgcctgaat aataaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa		1209
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa		1262
<210> 728		
<211> 229		
<212> PRT		
<213> Unknown Organism		
<220>		
<223> Description of Unknown Organism: 85P1B3/OIP5		
clone A protein		
<400> 728		
Met Ala Ala Gln Pro Leu Arg His Arg Ser Arg Cys Ala Thr Pro Pro		
1	5	10
		15

Arg Gly Asp Phe Cys Gly Gly Thr Glu Arg Ala Ile Asp Gln Ala Ser
 20 25 30

 Phe Thr Thr Ser Met Glu Trp Asp Thr Gln Val Val Lys Gly Ser Ser
 35 40 45

 Pro Leu Gly Pro Ala Gly Leu Gly Ala Glu Glu Pro Ala Ala Gly Pro
 50 55 60

 Gln Leu Pro Ser Trp Leu Gln Pro Glu Arg Cys Ala Val Phe Gln Cys
 65 70 75 80

 Ala Gln Cys His Ala Val Leu Ala Asp Ser Val His Leu Ala Trp Asp
 85 90 95

 Leu Ser Arg Ser Leu Gly Ala Val Val Phe Ser Arg Val Thr Asn Asn
 100 105 110

 Val Val Leu Glu Ala Pro Phe Leu Val Gly Ile Glu Gly Ser Leu Lys
 115 120 125

 Gly Ser Thr Tyr Asn Leu Leu Phe Cys Gly Ser Cys Gly Ile Pro Val
 130 135 140

 Gly Phe His Leu Tyr Ser Thr His Ala Ala Leu Ala Leu Arg Gly
 145 150 155 160

 His Phe Cys Leu Ser Ser Asp Lys Met Val Cys Tyr Leu Leu Lys Thr
 165 170 175

 Lys Ala Ile Val Asn Ala Ser Glu Met Asp Ile Gln Asn Val Pro Leu
 180 185 190

 Ser Glu Lys Ile Ala Glu Leu Lys Glu Lys Ile Val Leu Thr His Asn
 195 200 205

 Arg Leu Lys Ser Leu Met Lys Ile Leu Ser Glu Val Thr Pro Asp Gln
 210 215 220

 Ser Lys Pro Glu Asn
 225

<210> 729
 <211> 229
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: 85P1B3/OIP5
 protein sequence

<400> 729
 Met Ala Ala Gln Pro Leu Arg His Arg Ser Arg Cys Ala Thr Pro Pro
 1 5 10 15

Arg Gly Asp Phe Cys Gly Gly Thr Glu Arg Ala Ile Asp Gln Ala Ser
20 25 30

Phe Thr Thr Ser Met Glu Trp Asp Thr Gln Val Val Lys Gly Ser Ser
35 40 45

Pro Leu Gly Pro Ala Gly Leu Gly Ala Glu Glu Pro Ala Ala Gly Pro
50 55 60

Gln Leu Pro Ser Trp Leu Gln Pro Glu Arg Cys Ala Val Phe Gln Cys
65 70 75 80

Ala Gln Cys His Ala Val Leu Ala Asp Ser Val His Leu Ala Trp Asp
85 90 95

Leu Ser Arg Ser Leu Gly Ala Val Val Phe Ser Arg Val Thr Asn Asn
100 105 110

Val Val Leu Glu Ala Pro Phe Leu Val Gly Ile Glu Gly Ser Leu Lys
115 120 125

Gly Ser Thr Tyr Asn Leu Leu Phe Cys Gly Ser Cys Gly Ile Pro Val
130 135 140

Gly Phe His Leu Tyr Ser Thr His Ala Ala Leu Ala Ala Leu Arg Gly
145 150 155 160

His Phe Cys Leu Ser Ser Asp Lys Met Val Cys Tyr Leu Leu Lys Thr
165 170 175

Lys Ala Ile Val Asn Ala Ser Glu Met Asp Ile Gln Asn Val Pro Leu
180 185 190

Ser Glu Lys Ile Ala Glu Leu Lys Glu Lys Ile Val Leu Thr His Asn
195 200 205

Arg Leu Lys Ser Leu Met Lys Ile Leu Ser Glu Val Thr Pro Asp Gln
210 215 220

Ser Lys Pro Glu Asn
225

<210> 730
<211> 229
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 85P1B3 protein
sequence

<400> 730
Met Ala Ala Gln Pro Leu Arg His Arg Ser Arg Cys Ala Thr Pro Pro
1 5 10 15

Arg Gly Asp Phe Cys Gly Gly Thr Glu Arg Ala Ile Asp Gln Ala Ser

20

25

30

Phe Thr Thr Ser Met Glu Trp Asp Thr Gln Val Val Lys Gly Ser Ser
 35 40 45

Pro Leu Gly Pro Ala Gly Leu Gly Ala Glu Glu Pro Ala Ala Gly Pro
 50 55 60

Gln Leu Pro Ser Trp Leu Gln Pro Glu Arg Cys Ala Val Phe Gln Cys
 65 70 75 80

Ala Gln Cys His Ala Val Leu Ala Asp Ser Val His Leu Ala Trp Asp
 85 90 95

Leu Ser Arg Ser Leu Gly Ala Val Val Phe Ser Arg Val Thr Asn Asn
 100 105 110

Val Val Leu Glu Ala Pro Phe Leu Val Gly Ile Glu Gly Ser Leu Lys
 115 120 125

Gly Ser Thr Tyr Asn Leu Leu Phe Cys Gly Ser Cys Gly Ile Pro Val
 130 135 140

Gly Phe His Leu Tyr Ser Thr His Ala Ala Leu Ala Leu Arg Gly
 145 150 155 160

His Phe Cys Leu Ser Ser Asp Lys Met Val Cys Tyr Leu Leu Lys Thr
 165 170 175

Lys Ala Ile Val Asn Ala Ser Glu Met Asp Ile Gln Asn Val Pro Leu
 180 185 190

Ser Glu Lys Ile Ala Glu Leu Lys Glu Lys Ile Val Leu Thr His Asn
 195 200 205

Arg Leu Lys Ser Leu Met Lys Ile Leu Ser Glu Val Thr Pro Asp Gln
 210 215 220

Ser Lys Pro Glu Asn
 225

<210> 731

<211> 229

<212> PRT

<213> Homo sapiens

<400> 731

Met Ala Ala Gln Pro Leu Arg His Arg Ser Arg Cys Ala Thr Pro Pro
 1 5 10 15

Arg Gly Asp Phe Cys Gly Gly Thr Glu Arg Ala Ile Asp Gln Ala Ser
 20 25 30

Phe Thr Thr Ser Met Glu Trp Asp Thr Gln Val Val Lys Gly Ser Ser
 35 40 45

Pro Leu Gly Pro Ala Gly Leu Gly Ala Glu Glu Pro Ala Ala Gly Pro
50 55 60

Gln Leu Pro Ser Trp Leu Gln Pro Glu Arg Cys Ala Val Phe Gln Cys
65 70 75 80

Ala Gln Cys His Ala Val Leu Ala Asp Ser Val His Leu Ala Trp Asp
85 90 95

Leu Ser Arg Ser Leu Gly Ala Val Val Phe Ser Arg Val Thr Asn Asn
100 105 110

Val Val Leu Glu Ala Pro Phe Leu Val Gly Ile Glu Gly Ser Leu Lys
115 120 125

Gly Ser Thr Tyr Asn Leu Leu Phe Cys Gly Ser Cys Gly Ile Pro Val
130 135 140

Gly Phe His Leu Tyr Ser Thr His Ala Ala Leu Ala Ala Leu Arg Gly
145 150 155 160

His Phe Cys Leu Ser Ser Asp Lys Met Val Cys Tyr Leu Leu Lys Thr
165 170 175

Lys Ala Ile Val Asn Ala Ser Glu Met Asp Ile Gln Asn Val Pro Leu
180 185 190

Ser Glu Lys Ile Ala Glu Leu Lys Glu Lys Ile Val Leu Thr His Asn
195 200 205

Arg Leu Lys Ser Leu Met Lys Ile Leu Ser Glu Val Thr Pro Asp Gln
210 215 220

Ser Lys Pro Glu Asn
225

<210> 732
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 732
catgggactc tgcatcttaa ttcc 24

<210> 733
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 733
caggttcagg ctttattgct gtct

24

<210> 734
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic FLAG tag

<400> 734
gattacaagg atgacgacga taag

24

<210> 735
<211> 4
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: N-glycosylation site motif

<400> 735
Asn Ala Ser Glu
1

<210> 736
<211> 4
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: casein kinase II phosphorylation site motif

<400> 736
Thr Ser Met Glu
1

<210> 737
<211> 4
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: casein kinase II phosphorylation site motif

<400> 737
Ser Glu Met Asp
1

<210> 738
<211> 4
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: casein kinase II phosphorylation site motif

<400> 738
Ser Lys Pro Glu
1

<210> 739
<211> 6
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: N-myristoylation site motif

<400> 739
Gly Thr Glu Arg Ala Ile
1 5

<210> 740
<211> 6
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: N-myristoylation site motif

<400> 740
Gly Ile Glu Gly Ser Leu
1 5

<210> 741
<211> 6
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: N-myristoylation site motif

<400> 741
Gly Ser Leu Lys Gly Ser
1 5

<210> 742

<211> 6

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: N-myristoylation
site motif

<400> 742

Gly Ser Thr Tyr Asn Leu
1 5

<210> 743

<211> 6

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: N-myristoylation
site motif

<400> 743

Gly Ile Pro Val Gly Phe
1 5

<210> 744

<211> 6

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: cytochrome c
family heme-binding site motif

<400> 744

Cys Ala Gln Cys His Ala
1 5

1

1